

QY 302 SCLVLVLRQKRESLGKKRPHLCNVPDLITLHGISTVDSPLRYMLPHLVSTI-- 359  
 Db 298 LLLVCITGKO-----QALPHF--KPE--TLLNVGKKMLISTLSSIAKGNIAIOSICM 347  
 QY 360 ----HYVTGETBEGMDGOIYKRNHEALITKISLKNNDHLASLIFEEYIS----- 406  
 Db 348 PLMTGVAARDDASSNSCLFLDNLSEVPMKPTAOQLINCLODYVETALDAPBPM 407  
 QY 407 -----YSGQEBMSNKVSLNEOPLPLRLLESKYPTLVDVLEEHKEIADL 454  
 Db 408 ETNSNEDDITVIOSDDEIETEKTT--FQAWYSTLEKLERRYPEAFDLSVEKALRSKST 466  
 QY 455 KXOELPHQFV---SLTSGGKYOFPLADSDTSLMSTLNHPRLPVRLLANNH--LKKIMTKSK 510  
 Db 467 SNRQKALALGFRNLNTDEKAKAYE-----KLHYHSADWRLSAVQKLLQNLNVTYK 519  
 QY 511 EGVDESEFKEAVLARLDNDIVLSAIS--APEIFKEHSEBVTISNLTNFORAELSKN 569  
 Db 520 RERSVKLQECLEPRINDSGAVSTLSLPTBELAEMGLPLAQTLCHLLYRAQSKED 579  
 QY 570 GEWEVULKIADILIKEIISENDQSNQVVCILPVRVINDDTESAKMKIAYLSKSG 629  
 Db 580 EEMOPVPLAVRHLTSLVSGSYD--TLLVLLALMPLFPGEALAEHQKALRIILG--SD 636  
 QY 630 ICSLHPLLRGWEALENVIKSTKPKGLIGVANOIMIELLA--DNINLGDS--SMLKMWEDL 687  
 Db 637 FVSVKVPFLA--ELKVSNNKPSDFN---VGEHRQHPDLDIASSNOELSGOERALLQSYED- 689  
 QY 688 ISVGEESFNKOKATFHVILSVLSCSSIKETHPPAIRVFSILQKIKESVITAV 747  
 Db 690 --HGGELIYQKASOLT--HLLLLLTAVAKRELQPRESLHMLEKIGIYSRLQ--FRVYNGS 744  
 QY 748 E----IPSEWHIELMDRGIPELMAHYBELNSTORAVESVFLVFSIKFTI---Y 798  
 Db 745 QMTPNCAPLOLYVFLTLT--VKNTKWT---ALASTPMNQMTDELRLCLRIELIICQVFE 799  
 QY 799 ALKAPKSPKGDIMWNPQO-----LKGDSRUYLLLLGLFEMMLNGADAVHFRVLKLF 853  
 Db 800 SEKADQ--PERQENTRALQOSLOLILPEAQDRLDVLSN----- 835  
 QY 854 KVLHEDVFOLEKFCSSVLTGSSLSNPLNCSVKTVLQTOALVYGCAMLSQKTOCKHQLA 913  
 Db 836 -----FYPERBELMPPRSDYA-----VFRLQGFILIEAVLSNKGQIDGCV 879  
 QY 914 SISSPVVTSLLINSGPVKEVRRALAOCLQALSG--VASPYYLIIDHLISKABEITSDAA 971  
 Db 880 H-----VLAVANAGCSPLQTLRVOAINTLQILSNRKLVSHEQVRSLLQKSELSMDHE 934  
 QY 972 YVIODLATLPEBLOREKLSHQSLSETLKNLSCTVSCPS---YIAKDLAKVLOQYNGE 1028  
 Db 935 ---QYALILYTLLEPEKATAKERLVLSKLRKSVLALASDPKQSPICTAASLLAALKHVND 991  
 QY 1029 MVLSQLPMAEQLEKIOKEPTAVLKDBAMVHLTLGKNPSPVSLN--EDPKSLDIFI 1086  
 Db 992 NPLNELPLPLGDSIKTI-----TAGEDNQNIKHLR--WPHSITYSVIEREGRALANVL 1045  
 QY 1087 K-----AVHTKELVAGMPTIOITALLEKTKPFAAISDEKVOOK---LIR 1129  
 Db 1046 RKDLAMWLPEDSFAQDYTVVLEQKLOPLCVLINSILPTETF-----EOMHAKKIALIK 1100  
 QY 1130 MLPLDLVNCNKHQAQVSSVFKGISVNAEOVRLELBRPKAKPLGVYQOGRKXMOOK 1189  
 Db 1101 LIVESATNSDN-----DSLFLASHRLKRCRDLDCP--LVPILLEANNTKVEKKOPVK 1151  
 QY 1190 SODELSVQ--EYGSVMORVTLTLELQHKKLRSFQILVPTLPMILSRCLPELPOEQNM 1248  
 Db 1152 RRSVQAQODULSTSYWQGMTLLELHKQILGABELLIPFLFELLQACL--TMEHSISA 1299  
 QY 1249 EYTKQILSLCLNLCQKLSPPDGKI PRODILDEKPNVELLYQCIKRLSEMPOTNRHALLL 1308  
 Db 1210 EYKPOLITSLHCCQTAQASGVOLVK--AMPESFRLELVVQDSJRNTRNPTQOHALFL 1268  
 QY 1309 GTYAGIFPDKVLYNINMISITFMGMANVRLDDTYSFQVINTVKNVITALLIOSDSGDSIEV 1368

Db 1269 THCGMTPOQVLRHIVETIFFVGVSTVARHDDAFLSHIHNVBSITPIL-----L 1319  
 QY 1369 SRNVEIIVNVIISVFDALPVEHRLPLIVOLVDTLGAKEFLMILLILFEQYVTKV 1428  
 Db 1320 NTGNELVIVLVKVFADICIDVFNHRLPLIATLFLRLPEKHEHMQFLCIIFE-----SQV 1375  
 QY 1429 LAAAYGEKADILLEADTEFWFSVCCSFVSQHO-----IOSLNILOYLKLPKEEETPK 1483  
 Db 1376 LLREQVQKVSITDSKRDPE-----ARELTMEDPTVALQOTICRLDYLAKLPATKSLSGG 1431  
 QY 1484 AVSFNKSQOEMLQVNVETHYSKOLRHKFLSVSPMSOLSSNNFLKKVSGSGPEIL 1543  
 Db 1432 SGSSVLTBQO-----QLFDVATRTFKOLRHKLYLIMPLDSSISCSNENKMKRPDRELL 1487  
 QY 1544 KGLEERLETVLGYISAVQSMERNADKLV--KRWALLSKAYDLDRKVALLPETETIP 1602  
 Db 1488 PYOEFILKT--LAVGVTLNGALBAASETPSELKFMVRLANHAHDVLDNAILGLAPQHFLS 1546  
 QY 1603 VIRGLVNPPLPSVRKALDLNKLQONISW--KTIIVTRPLKVPDLIAIVO--RKKEG 1659  
 Db 1547 VITELRGHDVVYRIKMDLVLTKLSTSDYFOOSNAHFGVLPAPLOEIIINGIIQSSN 1606  
 QY 1660 EEEQAINROTALYTLKLCNFGAENDPFVPLXTAVKLIAPERKEKNVLSGALCIA 1719  
 Db 1607 SAQAKIQQOTALHALQOLARHGRDYTECRSLATITKTKRANVPKAVGNVUTLV 1666  
 QY 1720 EYVSTLEBALIPLPSPIMPSILTTMNTSELSVSEVYLSAL-----ALQKV 1767  
 Db 1667 EICASLYKHALAQPKRAPOL-----TELLKQVHQMASLKQGPVYGVSTLVTAHLK 1719  
 QY 1768 VETLPHFISYLBGILSQVHLEKITSBMSASQANRLTSLKKT-----LA 1814  
 Db 1720 FKALPFLGPLYVDIIGGLARL-----SVOLENPOLLQDRTQVLRKOKLADVSAVA 1771  
 QY 1815 TTLAPRVLPAIKKTYKQ--TEKWKQNMCGPFM--SILOEHIGXMKKEELTSHOSQTAFL 1872  
 Db 1772 QGVBRILVPSKAPSSLEEQAYDELGMLMOQLLOSRHNSAOLQVODPLSELFL 1831  
 QY 1873 BALDFRAQSHSENDLEB--VGKTENCIDCLVAMVVKLSEVTRPFLFKFDMAKTEDAPK 1930  
 Db 1832 QALNFRLOVGLQORQVSDVEASITETFTVTLKLSFSPRMYSRVHKMA--LESTSR 1890  
 QY 1931 DRLLTFYNLADCIABKLGKFLTPAGHLVPRPADTLKOVNIISKDEAFPSSENDPEKCL 1990  
 Db 1891 ETRLTYFLTLNRILAEALKSFLVLPASDPVDSRSLTTEHNSIRPEFEVERREDVD---- 1946  
 QY 1991 LLOFLNCLYKIFLFDTOHHSKERAXALMMPILVDOLERNLG--GEKFORBVTGHLPCI 2049  
 Db 1947 LMAILLNTLHNVFLYCSDFINDHRENVLMPLVNOLENDLVGNESLQOVLST----CI 2002  
 QY 2050 ACFSVAMADDSLWKPLNYQILKTRDSSPKVREPAALITVALAEKLENYIVLLPESIFP 2109  
 Db 2003 ACFAVA--TNDVMMKQKNSQVLTLTRSNPEVRILAFNSCVALARUKGESYVALLPETFVF 2061  
 QY 2110 LAELMEDCESEVHQCKTIOLETVLGEPLQSY 2143  
 Db 2062 IAEILBEDHQVRKNTRTGVQOIELTILIGESVQKY 2095  
 RESULT 12  
 Q8CCT5  
 AC Q8CCT5 PRELIMINARY; PRT; 408 AA.  
 ID Q8CCT5  
 DT 01-MAR-2003 (TEMBUREI. 23, Created)  
 DT 01-MAR-2003 (TEMBUREI. 23, Last sequence update)  
 DT 01-MAR-2004 (TEMBUREI. 26, Last annotation update)  
 DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length  
 DE enriched library, clone:643040006 product:hypothetical Ark repeat  
 DE structure containing protein, full insert sequence.  
 GN Name=13001612Rik; Synonyms=BC019693;  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Mech. Enzymol. 103:19-44(1999).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;  
 RA The FANTOM Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata K., Hayata N., Sugahara Y., Shibata K., Itoh M.,  
 Komno H., Akiyama J., Nishii K., Natsunai T., Tashiro H., Harada A.,  
 Suni N., Ishii Y., Nakamura S., Ikegami T., Kashiwagi K.,  
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
 Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1157-1171(2000).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Natsunai T., Tashiro H., Itoh M.,  
 Komno H., Akiyama J., Nishii K., Natsunai T., Tashiro H., Harada A.,  
 Suni N., Ishii Y., Nakamura S., Ikegami T., Kashiwagi K.,  
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
 Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1157-1171(2000).  
 [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 Hayashizaki K., Hayata N., Hatanaka T., Hara A., Hashizume W.,  
 Horii F., Imotani K., Ishii Y., Itoh M., Kaga M., Kato M., Koyama S.,  
 Kouchi H., Kawai J., Kojima Y., Kondo S., Komno H., Nakamura M.,  
 Kouchi H., Kawai J., Kojima Y., Kondo S., Komno H., Nakamura M.,  
 Kouchi H., Kawai J., Kojima Y., Kondo S., Komno H., Nakamura M.,  
 Nishii K., Nomura K., Numazaki R., Ono M., Ohashi N., Okazaki Y.,  
 Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,  
 Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK032134; BAC27721.1;  
 DR MGD: MGI:2442524; B13001612R1k.  
 DR InterPro: IPR006938; ARM.  
 KW Hypothetical protein.  
 SQ SEQUENCE 408 AA; 4668 MW; 42AB9EB13CA3FE67 CRC64;

Query Match 17.8%; Score 1926; DB 2; Length 408;  
 Best Local Similarity 91.9%; Pred. No. 5, 2e-82;  
 Matches 375; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

1737 MPELITMKTSELVSEVYLIALALQKVETLPHRISPLVLEGLGVHLEKITSFM 1796

Db 1 MPELITMKTSELVSEVYLIALALQKVETLPHRISPLVLEGLGVHLEKITSFM 60  
 QY GSASQANIRLTSKKTLATTLAPRVLPAIKTKYQIEKWKMGPMISLOEHIGMK 1856  
 Db 61 GSASQANIRLTSKKTLATTLAPRVLPAIKTKYQIEKWKMGPMISLOEHIGMK 120  
 QY KEELTSHOSQVTAFFLEALDRAQSHSENDLEEVKTCNCIICLVANVVKLSVTPPLF 1916  
 Db 121 KEELTSHOSQVTAFFLEALDRAQSHSENDLEEVKTCNCIICLVANVVKLSVTPPLF 180  
 QY FKIDPMATKEDAPDRLLTFNLADCTAEKKGFTLPAGHLYVPADTLTXQVNIKTDE 1976  
 Db 181 FKIDPMATKEDAPDRLLTFNLADCTAEKKGFTLPAGHLYVPADTLTXQVNIKTDE 240  
 QY AFPSDENPEKCCLLQFLNCLYKIPFDTHFISKEKAYALMPLVDLENRLGSEK 2036  
 Db 241 AFPSDENPEKCCLLQFLNCLYKIPFDTHFISKEKAYALMPLVDLENRLGSEK 300  
 QY 2037 FOERTKHLIPCIAGFSVAMADSLWKPNTYQILKTRDSSPKYRFPALLTVLALAEKX 2096  
 Db 301 FOERTKHLIPCIAGFSVAMADSLWKPNTYQILKTRDSSPKYRFPALLTVLALAEKX 360  
 QY 2097 ENYIVLLEPSIPFLAEIMDECEVEHOCOKTIOQLTVLGEPLQSYF 2144  
 Db 361 ENYIVLLEPSIPFLAEIMDECEVEHOCOKTIOQLTVLGEPLQSYF 408  
 RESULT 13  
 ID 096B55 PRELIMINARY; PRT; 349 AA.  
 AC 096B55;  
 DT 01-DEC-2001 (TRMBLrel. 19, Created)  
 DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)  
 DE FLJ10359 protein.  
 GN Name=FLJ10359;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxId=9606;  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=ovary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
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 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hult S.W.,  
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 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield J.S.,  
 Krzywinski M.I., Skellern U., Small D.B., Schnerch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ovary;  
 RA Strausberg R.;  
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011983; AAH11983.1;  
 DR InterPro: IPR006938; ARM.  
 KW InterPro: IPR003577; HEAT.